

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BROWNING, Jeffrey
WARE, Carl

(ii) TITLE OF INVENTION: LYMPHOTOXIN-BETA, LYMPHOTOXIN-BETA
COMPLEXES, PHARMACEUTICAL PREPARATIONS AND THERAPEUTIC
USES THEREOF

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: c/o FISH & NEAVE
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(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10020

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US91/04588
(B) FILING DATE: 27-JUN-1991

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/544,862
(B) FILING DATE: 27-JUN-1990

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: HALEY Jr., James F.
(B) REGISTRATION NUMBER: 27,794
(C) REFERENCE/DOCKET NUMBER: B129CIPII

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 596-9000
- (B) TELEFAX: (212) 596-9090
- (C) TELEX: 14-8367

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| CTG CCG CTC GAG GGC AGG GGT CGG AGG CTC CAG CGG AGG GGT TCC CTC | 48 |
| Leu Gly Leu Glu Gly Arg Gly Arg Leu Gln Gly Arg Gly Ser Leu | |
| 1 5 10 15 | |
| CTG CTA CCT GIG GCA GGA GGC ACT TCT CTG GIG ACC TTC TTC CTG CGG | 96 |
| Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu Leu Leu Ala | |
| 20 25 30 | |
| GIG CCT ATC ACT GTC CTG CCT GIG CTG GGC TTA GIG CCC CAG GAT CAG | 144 |
| Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro Gln Asp Gln | |
| 35 40 45 | |
| GGA CGA CTC GTC ACG GAG ACG GGC GAC CCC GGG GCA CAG GGC CAG CAA | 192 |
| Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln Ala Gln Gln | |
| 50 55 60 | |
| GGA CTG CGG TTT CAG AAG CTG CCA GAG GAG GCA GAA ACA GAT CTC | 240 |
| Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu Thr Asp Leu | |
| 65 70 75 80 | |
| AGC CGC CGG CTC CCA GCT GGC CAC CTC ATA GGC GCT CGG CTG AAG CGG | 288 |
| Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro Leu Lys Gly | |
| 85 90 95 | |
| CAG CGG CTC GGC TGG GAG ACG AAG AAG GAA CAG CGG TTT CTG ACG AGC | 336 |
| Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe Leu Thr Ser | |
| 100 105 110 | |
| GGG ACC CAG TTC TCG GAC GGC GAG CGG CTC CGC CGG CAG GAC CGC | 384 |
| Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro Gln Asp Gly | |
| 115 120 125 | |

TM9SF3B-1 323040007

| | |
|---|-----|
| CTC TAT TAC CTC TAC TGT CTC GTC GCC TAC CGG CTC CGG CGG CGC Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg Ala Pro Pro 130 135 140 | 432 |
| CGC CGC CGG GAC CGC CAG GCC CGC TCG GTC ACG CTG CGC AGC TCT CTC Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg Ser Ser Leu 145 150 155 160 | 480 |
| TAC CGG CGG CGC GCC TAC CGG CGC ACT CGC GAG CTG CTG CTC Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu Leu Leu 165 170 175 | 528 |
| GAG CGC GCC GAG ACG GIG ACT CCA GIG CTG GAC CGC AGG AGA CAA Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala Arg Arg Gln 180 185 190 | 576 |
| GGG TAC CGG CCT CTC TGG TAC ACG AGC GIG GGG TTC CGC CGC CTG GIG Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly Gly Leu Val 195 200 205 | 624 |
| CAG CTC CGG AGG CGC GAG AGG GIG TAC GTC AAC ATC AGT CAC CGC GAT Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro Asp 210 215 220 | 672 |
| ATG GTG GAC TTC GCG AGA GGG AAG ACC TTC TTT GGG GCC GIG ATG GIG Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala Val Met Val 225 230 235 240 | 720 |
| GGG TGA Gly | 726 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| |
|---|
| Leu Gly Leu Glu Gly Arg Gly Arg Leu Gln Gly Arg Gly Ser Leu 1 5 10 15 |
| Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu Leu Ala 20 25 30 |
| Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro Gln Asp Gln 35 40 45 |
| Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln Ala Gln Gln 50 55 60 |

Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu Thr Asp Leu
65 70 75 80

Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro Leu Lys Gly
85 90 95

Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe Leu Thr Ser
100 105 110

Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro Gln Asp Gly
115 120 125

Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg Ala Pro Pro
130 135 140

Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg Ser Ser Leu
145 150 155 160

Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu Leu Leu
165 170 175

Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala Arg Arg Gln
180 185 190

Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly Gly Leu Val
195 200 205

Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro Asp
210 215 220

Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala Val Met Val
225 230 235 240

Gly

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTG GCC TTA GIG CCC CAG GAT CAG GGA GGA CTG GTA ACG GAG ACG GCC
Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala
1 5 10 15

| | |
|--|-----|
| GAC CCC GCG GCA CAG GCC CAG CAA GCA CTC GCG TTT CAG AAG CTC CCA Asp Pro Gly Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro | 96 |
| 20 25 30 | |
| GCG GAG GAG CCA GAA ACA GAT CTC ACC CCC CGG CTC CCA GCT GCC CAC Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His | 144 |
| 35 40 45 | |
| CTC ATA GGC GCT CGG CTC AAG GGG CAG GGG CTC GGC TGG GAG ACC AGC Leu Ile Gly Ala Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr | 192 |
| 50 55 60 | |
| AAG GAA CAG GCG TTT CTC ACC GGC AGG CAG TTC TCG GAC GCC GAG Lys Glu Gln Ala Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu | 240 |
| 65 70 75 80 | |
| GGG CTG GCG CTC CGG CAG GAC GCC CTC TAT TAC CTC TAC TGT CTC GTC Gly Leu Ala Leu Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val | 288 |
| 85 90 95 | |
| GGC TAC CGG GGC CGG GCG CCC CCT GGC GGC GGG GAC CCC CAG GGC CGC Gly Tyr Arg Gly Arg Ala Pro Pro Gly Gly Asp Pro Gln Gly Arg | 336 |
| 100 105 110 | |
| TGG GTC ACG CTG CGC AGC TCT CTC TAC CGG CGG GGG GGC GCC TAC GGG Ser Val Thr Leu Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly | 384 |
| 115 120 125 | |
| CGG GGC ACT CCC GAG CTG CTG CTC CGG GGC GCC GAG ACG GIG ACT CCA Pro Gly Thr Pro Glu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro | 432 |
| 130 135 140 | |
| GIG CTG GAC CGG GCC AGG AGA CAA GGG TAC GGG CCT CTC TGG TAC ACG Val Leu Asp Pro Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr | 480 |
| 145 150 155 160 | |
| AGC GIG GGG TTC GGC GGC CTG GIG CAG CTC CGG AGG GGC GAG AGG GIG Ser Val Gly Phe Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val | 528 |
| 165 170 175 | |
| TAC GTC AAC ATC AGT CAC CCC GAT ATG GIG GAC TTC CGG AGA GGG AAG Tyr Val Asn Ile Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys | 576 |
| 180 185 190 | |
| ACC TTC TTT GGG GCC GIG AIG GIG GGG TGA Thr Phe Phe Gly Ala Val Met Val Gly | 606 |
| 195 200 | |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala
1 5 10 15

Asp Pro Gly Ala Gln Ala Gln Gly Leu Gly Phe Gln Lys Leu Pro
20 25 30

Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His
35 40 45

Leu Ile Gly Ala Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr
50 55 60

Lys Glu Gln Ala Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu
65 70 75 80

Gly Leu Ala Leu Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val
85 90 95

Gly Tyr Arg Gly Arg Ala Pro Pro Gly Gly Asp Pro Gln Gly Arg
100 105 110

Ser Val Thr Leu Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly
115 120 125

Pro Gly Thr Pro Glu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro
130 135 140

Val Leu Asp Pro Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr
145 150 155 160

Ser Val Gly Phe Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val
165 170 175

Tyr Val Asn Ile Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys
180 185 190

Thr Phe Phe Gly Ala Val Met Val Gly
195 200

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..447

100-00000000-110204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|--|-----|
| CGG CTC AAG GGG CAG GGG CTA GGC TCG GAG ACG AAG GAA CAG CGG Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala | 48 |
| 1 5 10 15 | |
| TTC CTC ACG AGC GGG ACG CAG TTC TCG GAC GGC GAG GGG CTC CGG CTC Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu | 96 |
| 20 25 30 | |
| CGG CAG GAC GGC CTC TAT TAC CTC TAC TGT CTC GTC GGC TAC CGG GGC Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly | 144 |
| 35 40 45 | |
| CGG CGG CCC CCT GGC GGC GGG GAC CCC CAG GGC CGC TCG GTC ACG CTC Arg Ala Pro Pro Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu | 192 |
| 50 55 60 | |
| CGC AGC TCT CTC TAC CGG CGG GGC GGC TAC GGG CGG CGC ACT CCC Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro | 240 |
| 65 70 75 80 | |
| GAG CTC CTC GAG GGC GGC GAG ACG GTG ACT CCA GTG CTC GAC CGG Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro | 288 |
| 85 90 95 | |
| GCC AGG AGA CAA GGG TAC GGG CCT CTC TGG TAC ACG AGC GTG GGG TTC Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe | 336 |
| 100 105 110 | |
| GCC CGC CTC GTG CAG CTC CGG AGG GGC GAG AGG GTG TAC GTC AAC ATC Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile | 384 |
| 115 120 125 | |
| AGT CAC CCC GAT ATG GTG GAC TTC GCG AGA GGG AAG AAG ACC TTC TTT GGG Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly | 432 |
| 130 135 140 | |
| GCC GTG ATG GTG GGG TGA Ala Val Met Val Gly | 450 |
| 145 | |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala
1 5 10 15

Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu
20 25 30

Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly
35 40 45

Arg Ala Pro Pro Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu
50 55 60

Arg Ser Ser Leu Tyr Arg Ala Gly Ala Tyr Gly Pro Gly Thr Pro
65 70 75 80

Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro
85 90 95

Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe
100 105 110

Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile
115 120 125

Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly
130 135 140

Ala Val Met Val Gly
145

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTG GCC TTA GIG CCC CAG GAT CAG CGA CGA CTG GIA ACG GAG ACG GCC
1 5 10 15

48

GAC CCC CGG GCA CAG GCC CAG CAA CGA CGA CTG CGG TTT CAG AAG CTG CCA
20 25 30

96

GAG GAG GAG CCA GAA ACA GAT CTC AGC CCG GTC CCA GCT GCC CAC 144
Glu Glu Glu Pro Glu Thr Asp Ile Ser Pro Gly Ile Pro Ala Ala His
35 40 45

CTC ATA GGC GCT 156
Ile Ile Gly Ala
50

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ile Ala Ile Val Pro Gln Asp Gln Gly Gly Ile Val Thr Glu Thr Ala
1 5 10 15

Asp Pro Gly Ala Gln Ala Gln Gly Ile Gly Phe Gln Lys Ile Pro
20 25 30

Glu Glu Glu Pro Glu Thr Asp Ile Ser Pro Gly Ile Pro Ala Ala His
35 40 45

Ile Ile Gly Ala
50

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTATCGGCT CYTCYTC

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTYTGTGGGT CTCCTTC

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGGGGCAC TGGGGCTG

18

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /function= "linker"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "The 5' terminal 4 nucleotides in the complementary strand are not present in this linker "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

cccccccccTTAGACCCACA

19

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACAGTGATA GGCAOOGCCA GCAACAA

27